

IN THE CLAIMS:

Please amend claim 12 as indicated in the following listing of the entire claims in the Application.

1. (Previously presented) A method for assembling nucleic acid base sequences comprising the steps of:
 - providing a plurality of nucleic acid base sequences;
 - moving an alignment window of a fixed base length along a first nucleic acid base sequence of the plurality of nucleic acid base sequences to define a first fixed-length sequence and simultaneously searching for a second nucleic acid base sequence having a terminal region matching exactly with the window of fixed base length;
 - determining whether the second nucleic acid base sequence and the first nucleic acid base sequence can be assembled or not by comparing a sequence adjacent to the aligned window of said first nucleic acid base sequence with a sequence adjacent to the aligned window of said second nucleic acid base sequence; and
 - assembling said first nucleic acid base sequence and said second nucleic acid base sequence if the sequences adjacent to the aligned windows are similar.
2. (Previously presented) A method for assembling nucleic acid base sequences according to claim 1, wherein the nucleic acid base sequence assembled in said assembling step is used as a reconstructed first nucleic acid base sequence to repeatedly carry out said moving, determining, and assembling steps.
3. (Previously presented) A method for assembling nucleic acid sequences comprising the steps of:
 - providing a plurality of nucleic acid base sequences;
 - entering identification information of each of the plurality of nucleic acid base sequences and the respective fixed base length sequence located in a terminal region of each of the nucleic acid base sequences into a table;
 - constructing a first consensus sequence based on a first nucleic acid base sequence of the plurality of nucleic acid base sequences;
 - searching the table for a second nucleic acid base sequence among remaining ones of the plurality of nucleic acid base sequences which shares a fixed length

sequence;

determining if the first nucleic acid base sequence and the second nucleic acid base sequence can be assembled by comparing the consensus and the second sequence where they are aligned at the exactly matching fixed length sequence; and if similar assembling said consensus sequence and second nucleic acid base sequences to reconstruct a new consensus sequence to repeatedly carry out the searching and determination steps.

4. (Previously Presented) The method for assembling nucleic acid base sequences according to claim 3, wherein a sequence whose base length is the longest among the plurality of nucleic acid base sequences is selected as said first nucleic acid base sequence.

5. (Previously presented) A method for assembling nucleic acid base sequences comprising:

a first step of sorting a plurality of nucleic acid base sequences in descending order of sequence lengths;

a second step of entering, into a table, identification information of each of the plurality of nucleic acid base sequences and a respective pair of fixed base length partial sequences located in a terminal region thereof;

a third step of selecting one of the nucleic acid base sequences whose sequence length is the longest among the plurality of nucleic acid base sequences as a first consensus sequence;

a fourth step of moving a fixed base length alignment window along said first consensus sequence to define a first fixed-length partial sequence and simultaneously searching for a second nucleic acid base sequence among remaining ones of the plurality of partial nucleic acid base sequences which has an exact match with the fixed base length alignment window;

a fifth step of determining if the first partial sequence and the second sequence can be assembled by comparing the consensus sequence and the second sequence where they are aligned at the exactly matching fixed-length partial sequence;

a sixth step of assembling the consensus and second partial sequences to reconstruct a new consensus sequence,

wherein the fourth step to the sixth step are repeated until said fixed base

length alignment window completes the scanning throughout said reconstructed consensus sequence, and said third step to said sixth step are repeated until all of the plurality of nucleic acid base sequences are selected in the third or fourth step and compared in the fifth step.

6. (Previously presented) The method for assembling nucleic acid base sequences according to claim 3, further comprising a step of picking up more than two of said fixed-length partial sequences to be entered into said table for each of the plurality of nucleic acid base sequences.
7. (Previously presented) The method for assembling nucleic acid base sequences according to claim 3, further comprising the step of designating a range of the terminal region of said first nucleic acid base sequence from which said fixed base length partial sequences to be entered into said table is extracted.
8. (Previously presented) The method for assembling nucleic acid base sequences according to claim 3, wherein the base length of said fixed base length partial sequences to be entered into said table is between 10 bases to 32 bases.
9. (Previously presented) The method for assembling nucleic acid base sequences according to claim 3, further comprising the steps of:
 - specifying an upper limit c as an expected number of entries retrieved from said table of a fixed base length partial sequence located in different nucleic acid base sequences or different positions in the plurality of nucleic acid base, and
 - specifying a length s of fixed base length sequences to be entered into said table as an integer satisfying the following expression (1)
$$s \geq \frac{1}{2} \log \frac{KN}{c} \quad \dots (1)$$
 - where N is the number of said plurality of nucleic acid base sequences and K is the number of the fixed base length sequences selected from each of the plurality of nucleic acid base sequences.
10. (Cancelled)

11. (Previously presented) The method for assembling nucleic acid base sequences according to claim 3, wherein each of said fixed base length sequences is represented by a fixed number of computing words which are independent of the length of the fixed-length partial sequences.
12. (Currently amended) The method for assembling nucleic acid base sequences according to claim 3, wherein every entry which corresponds to a partial sequence having a frequency of occurrence beyond a parameter given by a user is deleted from said table. ~~any entry in said table is removed if a number of entries sharing an identical key therein is more than a previously specified number.~~
- 13-15. (Cancelled)
16. (Previously presented) The method of claim 1, wherein a greedy algorithm is used to compare the similarity between the sequence adjacent to the aligned window of said first partial nucleic acid base sequence with a sequence adjacent to the aligned window of said second partial nucleic acid base sequence.
17. (Previously presented). The method of claim 3, wherein a greedy algorithm is used to compare the similarity between the sequences adjacent to the sections of the first and second nucleic acid base sequences aligned with said consensus sequence.
18. (Previously presented) The method of claim 5, wherein a greedy algorithm is used to compare the similarity between the sequences adjacent to the sections of the first and second partial sequences aligned with said alignment window.